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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1482
; US-08-805-166-1

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alignment_scores:
    Quality: 2449.00      Length: 493
    Ratio: 5.091          Gaps: 0
    Percent Similarity: 97.566    Percent Identity: 93.103

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alignment_block:

US-09-069-228-2 x US-08-805-166-1

Align seg 1/1 to: US-08-805-166-1 from: 1 to: 1482

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1 ATGACCCGACGACGCGCTCCGACCTGAGCCTGCGCTCTCTGCTGCTG 50
17 AAlaAlaLeuLeuSerProGlyLeuLysCysValCysLeuLeuAl 34
51 ACTGCGCTCCGACCTGCGGCGAGCTGAGTGTGTGTCTTTGTGTG 100
34 SPSErSerAspPheThrCysGlnThrGlnGlyAlaCysTrpAlaSerVal 50
101 ATTCCTCAAACTTACCTGCGCAACCGAAGGAGCATGCTGGGCTCTTC 150
51 MetLeuThrAsnGlyLysGlnValLleLysSerCysValSerLeuPr 67
151 ATGCTAACCAAGGGAAGACAGGTGATCAATCGTCCCTCCCTCC 200
67 OGLeuAsnAlaGlnValPheCysHisSerSerAspAsnValThrLys 84
201 GGAACCTAAATGCTCAGCTCTCTCTCTCAGCTTCCACACAGCTGAC 250
84 hrgLysCysPheThrAspPheCysAsnAsnLleThrLysLysLeuPro 100
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117 eileThrValProValCysLeuLeuSerLleAlaLleMetLeuThrVal 134
351 TATCACTGACTGTTTGGCTCTCTCTCTCTCAGCTGAGCAATGCTAAC 400
351 rAlaLysGlnGlyArgGlnCysSerTrpAlaLysLysLysArgProAsn 150
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151 ValGlnGluProLeuSerGluCysAsnLeuValAsnAlaGlyLysThr 167
451 GTGGAGAACCACTGGCAGAGTACAGCTTGCATGCTGGAAGAAACCT 500
167 uLysAspLeuLleTrpAspValThrAlaSerGlySerGlySerGlyLeu 184
501 CAAGATGATGATTTATGATGACGCTCGGCTCGAGATCTGGCTGCG 550
184 rOleuLeuValGlnArgThrLleAlaArgThrLleValLeuGlnGluLe 200
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201 ValGlyLysGlyArgPheGlyGluValTrpHisGlyArgTrpCysGly 217
601 GTAGAAAGAGTGGTGTGGAGAGTGGCAGGAGATGCTGTGGAGA 650

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651 AGATGTGCGCTGTGAAAAATTTCTCTCCAGAGATGAGAGATCTGTGTC 700
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701 GTGAGCGAGAAATTTATACAGCGGTAACTGAGACATGAGAAATATCTC 750
251 GlyPheLleAlaAlaAspAsnLysAspAsnGlyThrTrpThrGlnLeu 267
751 GGTTCATCCGCGCCGACAAACAAGATATGAAACCTGACCTAGCTTTG 800
267 PleuValSerGluTrpHisGlnGlnLysSerLeuTrpAspTrpLeuAsn 284
801 GCTGTGTGAGAGTATCAGACAGAGGCTCTTATATGACTATTGCAATA 850
284 rAsnLleValThrValAlaGlyMetLleLysLeuAlaLeuSerLleAla 300
851 GAACATAGTACCGCGCTGCGATGTCAGTGTGCGCTTCAATAGCG 900
301 SerGlyLeuAlaHisLysMetGluLleValGlyThrGlnGlyLysPr 317
901 AGTGTCTGCGCTCACCTACATGAGATCGTGGCCTCAAGGTAAAGCC 950
317 GalLleAlaHisArgAspLleLysSerLysAsnLleLeuValLysLysC 334
951 TGCTATCTCTACCGAGATATTAAGTCAAAAGATCTTACTAGCAAAAGT 1000
334 ysgLuthCysAlaLleAlaAspLeuGlyLeuAlaValLysHisAspSer 350
1001 GTGACACTGTGGCTAGCTAGCTAGCTGAGCTGCTGTCMAACATGATCT 1050
351 IleuAsnThrLleAspLleProGlnAsnProLysValGlyThrLysAr 367
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384 luserPheLysArgAlaAspLleLysSerValGlyLeuValTrpGlu 400
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401 IleAlaArgArgCysSerValGlyGlyLleValGlnGluLysLeuArg 417
1201 ATAGTCGGAAGGTGTCACTTGGAGACTTTGTAAGAGTACCACTTGC 1250
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434 alValCysAspGlnLysPheArgProSerLleProAsnGlnTrpLys 450
1301 TCGTTTGGATGAGAACTCCACCAAAATCTCCAAACAGTGGCAAGC 1350
451 CysGluAlaLeuArgValMetGlyArgLleMetArgLysLysTrpTrpAl 467
1351 TGTGAGGGGCTCCGGCTATGAGAAATATGCTGAGTCTGTGTATGC 1400
467 aAsnGlyAlaAlaArgLeuThrAlaLeuArgLleLysLysThrLleSerG 484
1401 CAACGGGGCAGCTGCGCTGACCGGCTCGGCTGAGAGAACCATTTCTC 1450
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1451 AGCTGTGTGTCAGAGACATGTAAGGCC 1479

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seq_name: /cgn2_6/prodata/2/lna/5b_COMB.seq:US-08-805-169-1

seq_documentation_block:

; Sequence 1, Application US/08805169
; Patent No. 5811245

GENERAL INFORMATION:
APPLICANT: Id ez, Carlos F.
APPLICANT: Ryd n, Mikael
APPLICANT: J Invall, Henrik
TITLE OF INVENTION: A No. 5811245el Serine Threonine Kinase Receptor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,169
FILING DATE: 24-FEB-1997
CLASSIFICATION: 536
FOR APPLICATION DATA:
APPLICATION NUMBER: 08/341,916
FILING DATE: 15-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1459, 0230001
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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1 MetThrArgAlaLeuCySerAlaLeuArgGlnAlaLeuLeuLeuAla 17
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17 aa1aa1aa1aa1aa1aa1aa1aa1aa1aa1aa1aa1aa1aa1aa 34
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